DNA BARCODING IN EUROPEAN AND AFRICAN *ACCIPITER* (ACCIPITRIDAE: FALCONIFORMES)

Breman FC[1], Sonet G[2], Nagy ZT[2], Jordaens K[1] & Louette M[1]

1. Royal Museum for Central Africa and JEMU. Leuvensesteenweg 13, B-3080, Tervuren, Belgium
2. Royal Belgian institute for Natural Sciences and JEMU. Vautierstraat 29, B-1000, Brussel, Belgium
3. Royal Belgian institute for Natural Sciences, ornithology section
4. Royal Museum for Central Africa, ornithology section

Introduction

DNA barcoding aims at using a standard 647bp fragment of the mitochondrial cytochrome *c* oxidase subunit I (COI) gene to identify species. Unfortunately, DNA of museum specimens is often degraded. Therefore, smaller fragments of the COI gene are used as mini-barcodes. Here, we compared the identification success of the standard (BC) and mini-barcode (mini-BC) fragment in a group of cosmopolitan raptors.

Material & methods

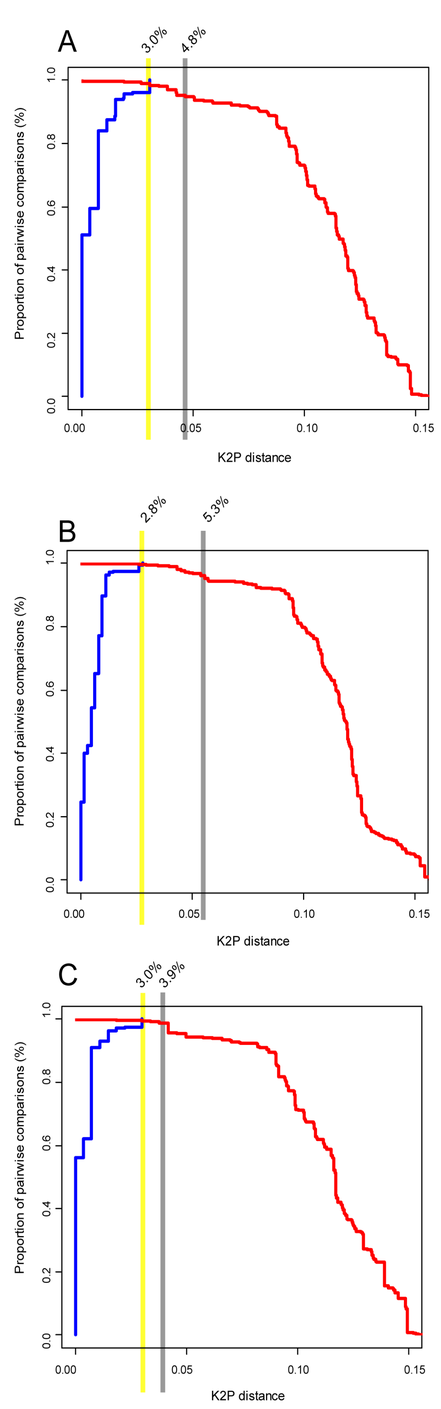
- 25 European and African *Accipiter* species
- 140 specimens

- three datasets: A: 25 species, 291bp,
  B: 19 species, 647bp,
  C: 19 species, 291bp

Century old photo of *Accipiter* (then *Astur*) *castanilius*

- intra- and interspecific sequence divergence: K2P distances
- Identification based on:
  best match (BM) criterion,
  best close match (BCM) criterion and
  character based identification
- thresholds using intra- and interspecific comparisons:
  10X mean intraspecific distance
  best compromise (BCo)

Examples of *Accipiter* skins used in this study



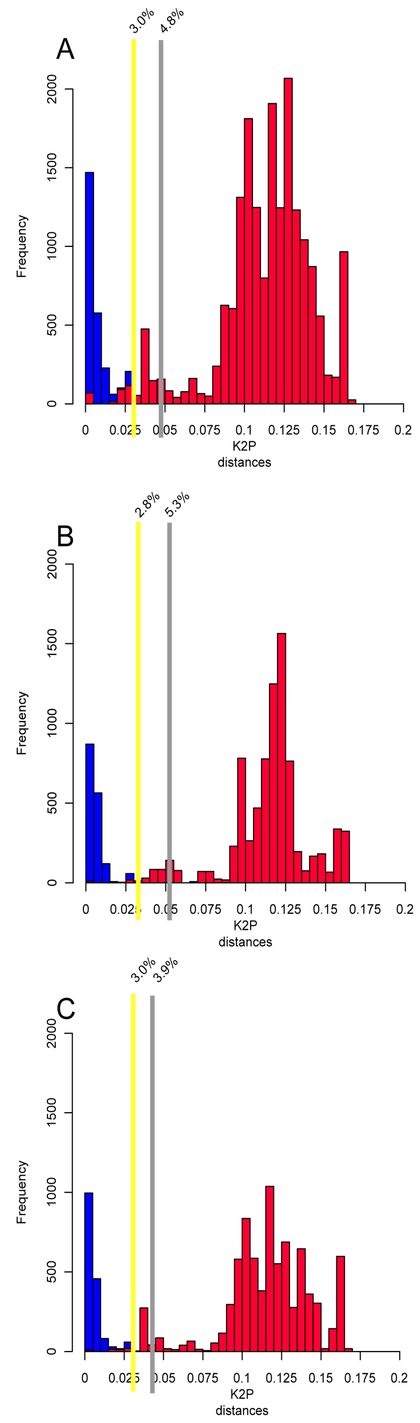


Figure 1:
Cumulative frequency graphs of intra (blue) and interspecific distances (red) for the three datasets A, B & C

Figure 2:
K2P distance distribution histograms with intra (blue) and interspecific distances (red) for the three datasets A, B & C

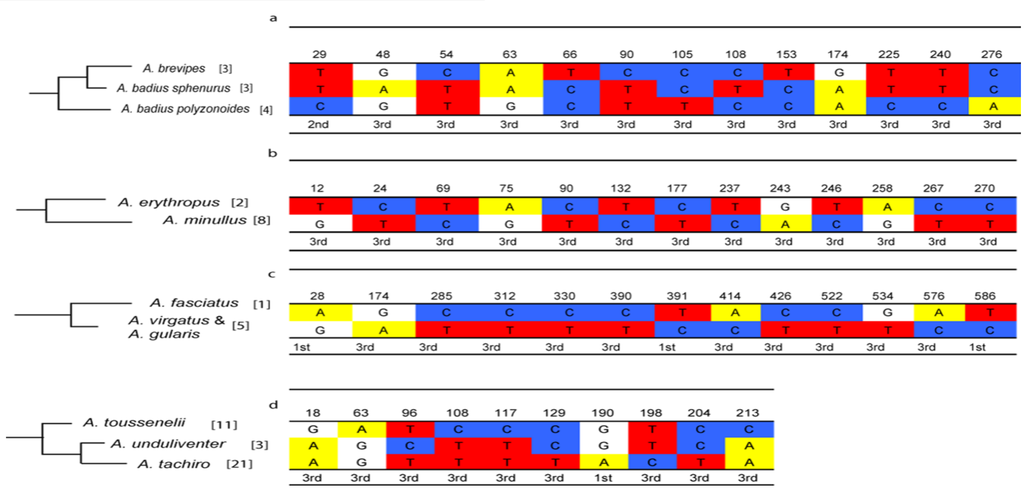


Figure 3:
Character state analysis for four closely related groups of *Accipiter* species

Results

- thresholds: 10X: 3-9% - 5.3% - BCo: 2.8% - 3.0 %
- identification success: standard BC: 90% - mini-BC: 84%
- BM and BCM criteria perform equally well

a BM

dataset	BCTh threshold	correct	ambiguous	incorrect	no match closer than threshold
A	3.00%	124 (84.35%)	19 (12.92%)	4 (2.72%)	–
B	2.80%	90 (90.0%)	6 (6.0%)	4 (4.0%)	–
C	3.00%	90 (90.0%)	5 (5.0%)	5 (5.0%)	–

b BCM

dataset	BCTh threshold	correct	ambiguous	incorrect	no match closer than threshold
A	3.00%	124 (84.35%)	18 (12.24%)	3 (2.04%)	2 (1.36%)
B	2.80%	90 (90.0%)	5 (5.0%)	4 (4.0%)	1 (1.0%)
C	3.00%	90 (90.0%)	5 (5.0%)	4 (4.0%)	1 (1.0%)

c BM

dataset	10 X threshold	correct	ambiguous	incorrect	no match closer than threshold
A	4.80%	124 (84.35%)	19 (12.92%)	4 (2.72%)	–
B	5.30%	90 (90.0%)	5 (5.0%)	5 (5.0%)	–
C	3.90%	90 (90.0%)	6 (6.0%)	4 (4.0%)	–

d BCM

dataset	10 X threshold	correct	ambiguous	incorrect	no match closer than threshold
A	4.80%	124 (84.35%)	18 (12.24%)	3 (2.04%)	2 (1.36%)
B	5.30%	90 (90.0%)	5 (5.0%)	4 (4.0%)	1 (1.0%)
C	3.90%	90 (90.0%)	5 (5.0%)	4 (4.0%)	1 (1.0%)

Table: identification successes and threshold values for the different methods and criteria used.

Conclusions

- 19 of the *Accipiter* species studied can be identified unambiguously using DNA barcoding
- six species (three species pairs) can not be identified using DNA barcoding
- the mini-BC performs slightly worse than the standard BC

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